

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lal, Preeti
Guegler, Karl J.
Corley, Neil C.

(ii) TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
(B) STREET: 3174 PORTER DRIVE
(C) CITY: PALO ALTO
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: CERRONE, MICHAEL C.
(B) REGISTRATION NUMBER: 39,132
(C) REFERENCE/DOCKET NUMBER: PF-0527 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 855-0555
(B) TELEFAX: (650) 845-4166

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSTUT10
(B) CLONE: 1691243

0937552660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met	Val	His	Val	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser	
				5					10					15	
Glu	Arg	Tyr	Leu	Phe	Leu	Asn	Met	Ala	Tyr	Gln	Gln	Val	His	Ala	
				20					25					30	
Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu	Val	Trp	Arg	Ile	Glu	
				35					40					45	
Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu	Ser	Leu	
				50					55					60	
Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp	
				65					70					75	
Arg	Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu	
				80					85					90	
Leu	Ile	Ser	Thr	Phe	His	Val	Leu	Ile	Tyr	Gly	Trp	Lys	Arg	Ala	
				95					100					105	
Phe	Glu	Glu	Glu	Tyr	Tyr	Arg	Phe	Tyr	Thr	Pro	Pro	Asn	Phe	Val	
				110					115					120	
Leu	Ala	Leu	Val	Leu	Pro	Ser	Ile	Val	Ile	Leu	Asp	Leu	Leu	Gln	
				125					130					135	
Leu	Cys	Arg	Tyr	Pro	Asp										
				140											

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT03
- (B) CLONE: 1999442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met	Phe	Leu	Pro	Pro	Val	Val	Leu	Ala	Ile	Arg	Ser	Arg	Tyr	Val	
				5					10					15	
Leu	Glu	Ala	Ala	Val	Tyr	Thr	Phe	Thr	Met	Phe	Phe	Ser	Thr	Phe	
				20					25					30	
Tyr	His	Ala	Cys	Asp	Gln	Pro	Gly	Ile	Val	Val	Phe	Cys	Ile	Met	
				35					40					45	
Asp	Tyr	Asp	Val	Leu	Gln	Phe	Cys	Asp	Phe	Leu	Gly	Ser	Leu	Met	
				50					55					60	
Ser	Val	Trp	Val	Thr	Val	Ile	Ala	Met	Ala	Arg	Leu	Gln	Pro	Val	
				65					70					75	
Val	Lys	Gln	Val	Leu	Tyr	Leu	Leu	Gly	Ala	Met	Leu	Leu	Ser	Met	
				80					85					90	
Ala	Leu	Gln	Leu	Asp	Arg	His	Gly	Leu	Trp	Asn	Leu	Leu	Gly	Pro	
				95					100					105	
Ser	Leu	Phe	Ala	Leu	Gly	Ile	Leu	Ala	Thr	Ala	Trp	Thr	Val	Arg	
				110					115					120	
Ser	Val	Arg	Arg	Arg	His	Cys	Tyr	Pro	Pro	Thr	Trp	Arg	Arg	Trp	
				125					130					135	
Leu	Phe	Tyr	Leu	Cys	Pro	Gly	Ser	Leu	Ile	Ala	Gly	Ser	Ala	Val	
				140					145					150	
Leu	Leu	Tyr	Ala	Phe	Val	Glu	Thr	Arg	Asp	Asn	Tyr	Phe	Tyr	Ile	

155 160 165
 His Ser Ile Trp His Met Leu Ile Ala Gly Ser Val Gly Phe Leu
 170 175 180
 Leu Pro Pro Arg Ala Lys Thr Asp His Gly Val Pro Ser Gly Ala
 185 190 195
 Arg Ala Arg Gly Cys Gly Tyr Gln Leu Cys Ile Asn Glu Gln Glu
 200 205 210
 Glu Pro Gly Pro Arg Gly Pro Arg Arg Gly His Cys Gln Gln His
 215 220 225
 Leu Cys Gln Leu Arg Gly Ala Leu Gly Leu Ala Leu Arg Gly Tyr
 230 235 240
 Glu Cys Phe Leu Glu Phe Phe Leu Gly Val Trp Ser Pro Leu Arg
 245 250 255
 Arg Arg Gln Ala Val Phe Leu Glu Asp Met Glu Ser Phe Ser Arg
 260 265 270
 Thr Gln Asn Ser Ser Arg Asp Leu Glu Pro Phe Pro Gly His Gly
 275 280 285
 Glu Leu Pro Glu Gly Leu Glu Ser Pro Cys Ile Met Glu Ser Phe
 290 295 300
 Leu Arg Thr Gly Ala Tyr Ala Gly Thr Glu Ser Leu Arg Thr Lys
 305 310 315
 Glu Ser Leu Leu Gln Val Trp Ser Leu Ser Trp Asp Ala Glu Pro
 320 325 330
 Ser Gln Asp Met Asp Ser Phe Pro Gly Arg Gln Ser Pro Val Arg
 335 340 345
 Ser Thr Ala Ser Phe Gln Arg Arg Trp Ser Leu Ser Trp Gly Asn
 350 355 360
 Gln Ile Ser Arg Phe Ser Gln Arg Leu Ser Asn Ser Gly Leu Arg
 365 370 375
 Leu Pro Ser Gln Arg Gln Arg Leu Gly Cys Ala Val Leu Trp Arg
 380 385 390
 Arg Asp Cys Arg Met Asp Gly Ala Gly Thr Gly Ala Val Trp Val
 395 400 405
 Ala Gly Ile Leu Val
 410

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT10
- (B) CLONE: 1691243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

CAAGTATAGG AGATTTCCAC CTTGGTTGGA AACCTGGTTA CAGTGTAGAA AACAGCTTGG 60
 ATTACTAAGT TTTTCTTCG CTATGGTCCA TGTTGCCTAC AGCCTCTGCT TACCGATGAG 120
 AAGGTCAGAG AGATATTTGT TTCTCAACAT GGCTTATCAG CAGGTTTCATG CAAATATTGA 180
 AAACCTCTGG AATGAGGAAG AAGTTTGGAG AATTGAAATG TATATCTCCT TTGGCATAAT 240
 GAGCCTTGGC TTA CTTTCCC TCCTGGCAGT CACTTCTATC CCTTCAGTGA GCAATGCTTT 300
 AAACCTGGAGA GAATTCAGTT TTATTCAGTC TACACTTGGA TATGTCGCTC TGCTCATAAG 360
 TACTTTCCAT GTTTTAATTT ATGGATGGAA ACGAGCTTTT GAGGAAGAGT ACTACAGATT 420
 TTATACACCA CCAAACCTTG TTCTTGCTCT TGTTTTGCC TCAATTGTAA TTCTGGATCT 480

TTTGCAGCTT TGCAGATACC CAGACTGAGC TGGAACTGGA ATTTGTCTTC CTATTGACTC 540
 TACTTCTTTA AAAGCGGCTG CCCATTACAT TCCTCAGCTG TCCTTGCACT TAGGTGTACA 600
 TGTGACTGAG TGTGGGCCAG TGAGATGAAG TCTCCTCAA GGAAGGCAGC ATGTGTCCTT 660
 TTTTCATCCCT TCATCTTGCT GCTGGGATTG TGGATATAAC AGGAGCCCTG GCAGCTGTCT 720
 CCAGAGGATC AAAGCCACAC CCAAAGAGTA AGGCAGATTA GAGACCAGAA AGACCTTGAC 780
 TACTTCCCTA CTTCCACTGC TTTTTCCTGC ATTTAAGCCA TTGTAAATCT GGGTGTGTTA 840
 CATGAAGTGA AAATTAATTC TTTCTGCCCT TCAGTTCTTT ATCCTGATAC CATTTAACAC 900
 TGTCTGAATT AACTAGACTG CAATAATTCT TTCTTTTGAA AGCTTTTAAA GGATAATGTG 960
 CAATTCACAT TAAAATTGAT TTTCCATTGT CAATTAGTTA TACTCATTTT CCTGCCTTGA 1020
 TCTTTCATTA GATATTTTGT ATCTGCTTGG AATATATTAT CTTCTTTTAA ACTGTGTAAT 1080
 TGGTAATTAC TAAAACCTCTG TAATCTCCAA AATATTGCTA TCAAATTACA CACCATGTTT 1140
 TCTATCATTC TCATAGATCT GCCTTATAAA CATTTAAATA AAAAGTACTA TTTAATGATT 1200
 TAAAAAAA AA 1213

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT03
 (B) CLONE: 1999442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

CGGACGCGTG GGCTGCTCTG CCTGAGCAAC CTCATGTTTC TGCCACCTGT GGTCTGGGCC 60
 ATTCGGAGTC GATATGTGCT GGAAGCTGCA GTCTACACCT TCACCATGTT CTTCTCCACG 120
 TTCTATCATG CCTGTGACCA GCCAGGCATC GTGGTTTTCT GCATCATGGA CTACGATGTG 180
 CTGCAGTTCT GTGATTTCTT GGGCTCCTTA ATGTCCGTGT GGGTCACTGT CATTGCCATG 240
 GCTCGTTTAC AGCCCGTGGT CAAGCAGGTG CTGTATTTGC TGGGAGCTAT GCTGCTGTCC 300
 ATGGCTCTGC AGCTTGACCG ACATGGACTC TGGAACCTGC TTGGACCCAG TCTCTTCGCC 360
 CTGGGGATCT TGGCCACAGC CTGGACAGTA CGCAGCGTCC GCCGCCGGCA CTGCTACCCA 420
 CCCACGTGGC GCCGCTGGCT TTTCTACTTG TGCCCTGGCA GCCTTATTGC AGGCAGTGCC 480
 GTCCTGCTTT ATGCTTTTGT GGAGACCCGG GACAACACT TCTACATTCA CAGCATTTGG 540
 CATATGCTCA TTGCGGGCAG TGTGGGCTTC CTGCTGCCCC CTCGTGCCAA GACTGACCAC 600
 GGGGTCCCAT CTGGAGCCCG GGCCCGGGGC TGTGGTTACC AGCTATGCAT CAACGAGCAG 660
 GAGGAGCCTG GGCTTCGTGG GCCCAGGAGG GGCCACTGTC AGCAGCATCT GTGCCAGCTG 720
 AGAGGGGCTT TGGGCCTGGC CCTGAGGGGA TATGAATGCT TCCTAGAGTT CTTTCTGGGG 780
 GTGTGGAGCC CTCTTAGAAG GAGACAGGCT GTATTTCTTG AGGACATGGA GTCTTTCTCA 840
 AGGACACAAA ACTCTTCCAG GGACCTGGAG CCCTTCCCAG GACATGGAGA ACTTCTTGAG 900
 GGCCTGGAGT CCCCCTGCAT CATGGAGTCC TTCTTAAGGA CTGGAGCCTA TGCAGGCACA 960
 GAGTCCCTCA GGACCAAGGA GTCCCTCCTG CAGGTGTGGA GCCTTTCCTG GGATGCAGAG 1020
 CCTTCCCAAG ACATGGATTC CTTCCCAGGG AGACAAAGCC CTGTCAGGAG CACAGCATCT 1080
 TTCCAGAGGA GGTGGAGTCT ATCTTGGGGA AACCAAATTT CCAGATTTTC CCAGAGGCTC 1140
 AGCAACTCTG GCCTCAGGCT TCCTTCCCAG AGGCAGCGTC TGGGCTGTGC TGTGCTGTGG 1200
 AGGAGGGATT GCAGGATGGA TGGAGCTGGG ACTGGGGCTG TCTGGGTGGC TGGTATCCTC 1260
 GTTTGATACA GGTGGAGTCT CTGTGTCTCC ATAGAAG 1297

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1216498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

Met	Gly	Arg	Ala	Met	Val	Val	Arg	Leu	Gly	Leu	Gly	Leu	Leu	Leu	
				5					10					15	
Leu	Ala	Leu	Leu	Leu	Pro	Thr	Gln	Ile	Tyr	Cys	Asn	Gln	Thr	Ser	
				20					25					30	
Val	Ala	Pro	Phe	Ser	Gly	Asn	Gln	Ser	Ile	Ser	Ala	Ala	Pro	Asn	
				35					40					45	
Pro	Thr	Asn	Ala	Thr	Thr	Arg	Ser	Gly	Cys	Ser	Ser	Leu	Gln	Ser	
				50					55					60	
Thr	Ala	Gly	Leu	Leu	Ala	Leu	Ser	Leu	Ser	Leu	Leu	His	Leu	Tyr	
				65					70					75	
Cys															

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 130989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

Met	Trp	Val	Pro	Val	Val	Phe	Leu	Thr	Leu	Ser	Val	Thr	Trp	Ile	
				5					10					15	
Gly	Ala	Ala	Pro	Leu	Ile	Leu	Ser	Arg	Ile	Val	Gly	Gly	Trp	Glu	
				20					25					30	
Cys	Glu	Lys	His	Ser	Gln	Pro	Trp	Gln	Val	Leu	Val	Ala	Ser	Arg	
				35					40					45	
Gly	Arg	Ala	Val	Cys	Gly	Gly	Val	Leu	Val	His	Pro	Gln	Trp	Val	
				50					55					60	
Leu	Thr	Ala	Ala	His	Cys	Ile	Arg	Asn	Lys	Ser	Val	Ile	Leu	Leu	
				65					70					75	
Gly	Arg	His	Ser	Leu	Phe	His	Pro	Glu	Asp	Thr	Gly	Gln	Val	Phe	
				80					85					90	
Gln	Val	Ser	His	Ser	Phe	Pro	His	Pro	Leu	Tyr	Asp	Met	Ser	Leu	
				95					100					105	
Leu	Lys	Asn	Arg	Phe	Leu	Arg	Pro	Gly	Asp	Asp	Ser	Ser	His	Asp	
				110					115					120	
Leu	Met	Leu	Leu	Arg	Leu	Ser	Glu	Pro	Ala	Glu	Leu	Thr	Asp	Ala	
				125					130					135	
Val	Lys	Val	Met	Asp	Leu	Pro	Thr	Gln	Glu	Pro	Ala	Leu	Gly	Thr	
				140					145					150	
Thr	Cys	Tyr	Ala	Ser	Gly	Trp	Gly	Ser	Ile	Glu	Pro	Glu	Glu	Phe	
				155					160					165	
Leu	Thr	Pro	Lys	Lys	Leu	Gln	Cys	Val	Asp	Leu	His	Val	Ile	Ser	
				170					175					180	
Asn	Asp	Val	Cys	Ala	Gln	Val	His	Pro	Gln	Lys	Val	Thr	Lys	Phe	
				185					190					195	

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Met	Leu	Cys	Ala	Gly	Arg	Trp	Thr	Gly	Gly	Lys	Ser	Thr	Cys	Ser	
				200					205					210	
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	Gly	Val	Leu	Gln	Gly	
				215					220					225	
Ile	Thr	Ser	Trp	Gly	Ser	Glu	Pro	Cys	Ala	Leu	Pro	Glu	Arg	Pro	
				230					235					240	
Ser	Leu	Tyr	Thr	Lys	Val	Val	His	Tyr	Arg	Lys	Trp	Ile	Lys	Asp	
				245					250					255	
Thr	Ile	Val	Ala	Asn	Pro										
				260											

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 2459993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

Met	Leu	Ala	Cys	Leu	Cys	Cys	Lys	Lys	Gly	Gly	Ile	Gly	Phe	Lys	
				5					10					15	
Glu	Phe	Glu	Asn	Ala	Glu	Gly	Asp	Glu	Tyr	Val	Ala	Asp	Phe	Ser	
				20					25					30	
Glu	Gln	Gly	Ser	Pro	Ala	Ala	Ala	Ala	Gln	Thr	Gly	Pro	Asp	Val	
				35					40					45	
Tyr	Val	Leu	Pro	Leu	Thr	Glu	Val	Ser	Leu	Pro	Met	Ala	Lys	Gln	
				50					55					60	
Pro	Gly	Arg	Ser	Val	Gln	Leu	Leu	Lys	Ser	Thr	Asp	Leu	Gly	Arg	
				65					70					75	
His	Ser	Leu	Leu	Tyr	Leu	Lys	Glu	Ile	Gly	His	Gly	Trp	Phe	Gly	
				80					85					90	
Lys	Val	Phe	Leu	Gly	Glu	Val	His	Ser	Gly	Val	Ser	Gly	Thr	Gln	
				95					100					105	
Val	Val	Val	Lys	Glu	Leu	Lys	Val	Ser	Ala	Ser	Val	Gln	Glu	Gln	
				110					115					120	
Met	Gln	Phe	Leu	Glu	Glu	Ala	Gln	Pro	Tyr	Arg	Ala	Leu	Gln	His	
				125					130					135	
Ser	Asn	Leu	Leu	Gln	Cys	Leu	Ala	Gln	Cys	Ala	Glu	Val	Thr	Pro	
				140					145					150	
Tyr	Leu	Leu	Val	Met	Glu	Phe	Cys	Pro	Leu	Gly	Asp	Leu	Lys	Gly	
				155					160					165	
Tyr	Leu	Arg	Ser	Cys	Arg	Val	Thr	Glu	Ser	Met	Ala	Pro	Asp	Pro	
				170					175					180	
Leu	Thr	Leu	Gln	Arg	Met	Ala	Cys	Glu	Val	Ala	Cys	Gly	Val	Leu	
				185					190					195	
His	Leu	His	Arg	His	Asn	Tyr	Val	His	Ser	Asp	Leu	Ala	Leu	Arg	
				200					205					210	
Asn	Cys	Leu	Leu	Thr	Ala	Asp	Leu	Thr	Val	Lys	Val	Gly	Asp	Tyr	
				215					220					225	
Gly	Leu	Ser	His	Cys	Lys	Tyr	Arg	Glu	Asp	Tyr	Leu	Val	Thr	Ala	
				230					235					240	
Asp	Gln	Leu	Trp	Val	Pro	Leu	Arg	Trp	Ile	Ala	Pro	Glu	Leu	Val	

Asp	Glu	Val	His	245	Gly	Asn	Leu	Leu	Val	250	Val	Asp	Gln	Thr	Lys	Ser	255
Ser	Asn	Val	Trp	260	Ser	Leu	Gly	Val	Thr	265	Ile	Trp	Glu	Leu	Phe	Glu	270
Leu	Gly	Ala	Gln	275	Pro	Tyr	Pro	Gln	His	280	Ser	Asp	Arg	Gln	Val	Leu	285
Ala	Tyr	Ala	Val	290	Arg	Glu	Gln	Gln	Leu	295	Lys	Leu	Pro	Lys	Pro	Gln	300
Leu	Gln	Leu	Ala	305	Leu	Ser	Asp	Arg	Trp	310	Tyr	Glu	Val	Met	Gln	Phe	315
Cys	Trp	Leu	Gln	320	Pro	Glu	Gln	Arg	Pro	325	Thr	Ala	Glu	Glu	Val	His	330
Leu	Leu	Leu	Ser	335	Tyr	Leu	Cys	Ala	Lys	340	Gly	Thr	Thr	Glu	Leu	Glu	345
Glu	Glu	Phe	Glu	350	Arg	Arg	Trp	Arg	Ser	355	Leu	Arg	Pro	Gly	Gly	Ser	360
Thr	Gly	Leu	Gly	365	Ser	Gly	Ser	Ala	Ala	370	Pro	Ala	Ala	Ala	Thr	Ala	375
Ala	Ser	Ala	Glu	380	Leu	Thr	Ala	Ala	Ser	385	Ser	Phe	Pro	Leu	Leu	Glu	390
Arg	Phe	Thr	Ser	395	Asp	Gly	Phe	His	Val	400	Ser	Asp	Asp	Val	Leu		405
Thr	Val	Thr	Glu	410	Thr	Ser	His	Gly	Leu	415	Asn	Phe	Glu	Tyr	Lys	Trp	420
Glu	Ala	Gly	Cys	425	Gly	Ala	Glu	Glu	Tyr	430	Pro	Pro	Ser	Gly	Ala	Ala	435
Ser	Ser	Pro	Gly	440	Ser	Ala	Ala	Arg	Leu	445	Gln	Glu	Leu	Cys	Ala	Pro	450
Asp	Ser	Ser	Pro	455	Pro	Gly	Val	Val	Pro	460	Val	Leu	Ser	Ala	His	Ser	465
Pro	Ser	Val	Gly	470	Ser	Glu	Tyr	Phe	Ile	475	Arg	Leu	Glu	Gly	Ala	Val	480
Pro	Ala	Ala	Gly	485	His	Asp	Pro	Asp	Cys	490	Ala	Gly	Cys	Ala	Pro	Ser	495
Pro	Gln	Ala	Val	500	Thr	Asp	Gln	Asp	Asn	505	Asn	Ser	Glu	Glu	Ser	Thr	510
Val	Ala	Ser	Leu	515	Ala	Met	Glu	Pro	Leu	520	Leu	Gly	His	Ala	Pro	Pro	525
Thr	Glu	Gly	Leu	530	Trp	Gly	Pro	Cys	Asp	535	His	His	Ser	His	Arg	Arg	540
Gln	Gly	Ser	Pro	545	Cys	Pro	Ser	Arg	Ser	550	Pro	Ser	Pro	Gly	Thr	Pro	555
Met	Leu	Pro	Ala	560	Glu	Asp	Ile	Asp	Trp	565	Gly	Val	Ala	Thr	Phe	Cys	570
Pro	Pro	Phe	Phe	575	Asp	Asp	Pro	Leu	Gly	580	Ala	Ser	Pro	Ser	Gly	Ser	585
Pro	Gly	Ala	Gln	590	Pro	Ser	Pro	Ser	Asp	595	Glu	Glu	Pro	Glu	Glu	Gly	600
Lys	Val	Gly	Leu	605	Ala	Ala	Gln	Cys	Gly	610	His	Trp	Ser	Ser	Asn	Met	615
Ser	Ala	Asn	Asn	620	Asn	Ser	Ala	Ser	Arg	625	Asp	Pro	Glu	Ser	Trp	Asp	630
Pro	Gly	Tyr	Val	635	Ser	Ser	Phe	Thr	Asp	640	Ser	Tyr	Arg	Asp	Asp	Cys	645
Ser	Ser	Leu	Glu	650	Gln	Thr	Pro	Arg	Ala	655	Ser	Pro	Glu	Val	Gly	His	660
Leu	Leu	Ser	Gln	665	Glu	Asp	Pro	Arg	Asp	670	Phe	Leu	Pro	Gly	Leu	Val	675
Ala	Val	Ser	Pro	680	Gly	Gln	Glu	Pro	Ser	685	Arg	Pro	Phe	Asn	Leu	Leu	690
				695						700							705

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Pro	Leu	Cys	Pro	Ala	Lys	Gly	Leu	Ala	Pro	Ala	Ala	Cys	Leu	Ile	710	715	720
Thr	Ser	Pro	Trp	Thr	Glu	Gly	Ala	Val	Gly	Gly	Ala	Glu	Asn	Pro	725	730	735
Ile	Val	Glu	Pro	Lys	Leu	Ala	Gln	Glu	Ala	Glu	Gly	Ser	Ala	Glu	740	745	750
Pro	Gln	Leu	Pro	Leu	Pro	Ser	Val	Pro	Ser	Pro	Ser	Cys	Glu	Gly	755	760	765
Ala	Ser	Leu	Pro	Ser	Glu	Glu	Ala	Ser	Ala	Pro	Asp	Ile	Leu	Pro	770	775	780
Ala	Ser	Pro	Thr	Pro	Ala	Ala	Gly	Ser	Trp	Val	Thr	Val	Pro	Glu	785	790	795
Pro	Ala	Pro	Thr	Leu	Glu	Ser	Ser	Gly	Ser	Ser	Leu	Gly	Gln	Glu	800	805	810
Ala	Pro	Ser	Ser	Glu	Asp	Glu	Asp	Thr	Thr	Glu	Ala	Thr	Ser	Gly	815	820	825
Val	Phe	Thr	Asp	Leu	Ser	Ser	Asp	Gly	Pro	His	Thr	Glu	Lys	Ser	830	835	840
Gly	Ile	Val	Pro	Ala	Leu	Arg	Ser	Leu	Gln	Lys	Gln	Val	Gly	Thr	845	850	855
Pro	Asp	Ser	Leu	Asp	Ser	Leu	Asp	Ile	Pro	Ser	Ser	Ala	Ser	Asp	860	865	870
Gly	Gly	Cys	Glu	Val	Leu	Ser	Pro	Ser	Ala	Ala	Gly	Pro	Pro	Gly	875	880	885
Gly	Gln	Pro	Arg	Ala	Val	Asp	Ser	Gly	Tyr	Asp	Thr	Glu	Asn	Tyr	890	895	900
Glu	Ser	Pro	Glu	Phe	Val	Leu	Lys	Glu	Ala	His	Glu	Ser	Ser	Glu	905	910	915
Pro	Glu	Ala	Phe	Gly	Glu	Pro	Ala	Ser	Glu	Gly	Glu	Ser	Pro	Gly	920	925	930
Pro	Asp	Pro	Leu	Leu	Ser	Val	Ser	Leu	Gly	Gly	Leu	Ser	Lys	Lys	935	940	945
Ser	Pro	Tyr	Arg	Asp	Ser	Ala	Tyr	Phe	Ser	Asp	Leu	Asp	Ala	Glu	950	955	960
Ser	Glu	Pro	Thr	Phe	Gly	Pro	Glu	Lys	His	Ser	Gly	Ile	Gln	Asp	965	970	975
Ser	Gln	Lys	Glu	Gln	Asp	Leu	Arg	Ser	Pro	Pro	Ser	Pro	Gly	His	980	985	990
Gln	Ser	Val	Gln	Ala	Phe	Pro	Arg	Ser	Ala	Val	Ser	Ser	Glu	Val	995	1000	1005
Leu	Ser	Pro	Pro	Gln	Gln	Ser	Glu	Glu	Pro	Leu	Pro	Glu	Val	Pro	1010	1015	1020
Arg	Pro	Glu	Pro	Leu	Gly	Ala	Gln	Gly	Pro	Val	Gly	Val	Gln	Pro	1025	1030	1035
Val	Pro	Gly	Pro	Ser	His	Ser	Lys	Cys	Phe	Pro	Leu	Thr	Ser	Val	1040	1045	1050
Pro	Leu	Ile	Ser	Glu	Gly	Ser	Gly	Thr	Glu	Pro	Gln	Gly	Pro	Ser	1055	1060	1065
Gly	Gln	Leu	Ser	Gly	Arg	Ala	Gln	Gln	Gly	Gln	Met	Gly	Asn	Pro	1070	1075	1080
Ser	Thr	Pro	Arg	Ser	Pro	Leu	Cys	Leu	Ala	Leu	Pro	Gly	His	Pro	1085	1090	1095
Gly	Ala	Leu	Glu	Gly	Arg	Pro	Glu	Glu	Asp	Glu	Asp	Thr	Glu	Asp	1100	1105	1110
Ser	Glu	Glu	Ser	Asp	Glu	Glu	Leu	Arg	Cys	Tyr	Ser	Val	Gln	Glu	1115	1120	1125
Pro	Ser	Glu	Asp	Ser	Glu	Glu	Glu	Pro	Pro	Ala	Val	Pro	Val	Val	1130	1135	1140
Val	Ala	Glu	Ser	Gln	Ser	Ala	Arg	Asn	Leu	Arg	Ser	Leu	Leu	Lys	1145	1150	1155
Met	Pro	Ser	Leu	Leu	Ser	Glu	Ala	Phe	Cys	Asp	Asp	Leu	Glu	Arg			

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	1160		1165		1170
Lys Lys Lys Ala Val	Ser Phe Phe Asp Asp	Val Thr Val Tyr Leu			
	1175		1180		1185
Phe Asp Gln Glu Ser	Pro Thr Arg Glu Thr	Gly Glu Pro Phe Pro			
	1190		1195		1200
Ser Thr Lys Glu Ser	Leu Pro Thr Phe Leu	Glu Gly Gly Pro Ser			
	1205		1210		1215
Ser Pro Ser Ala Thr	Gly Leu Pro Leu Arg	Ala Gly His Ser Pro			
	1220		1225		1230
Asp Ser Ser Ala Pro	Glu Pro Gly Ser Arg	Phe Glu Trp Asp Gly			
	1235		1240		1245
Asp Phe Pro Leu Val	Pro Gly Lys Ala Ala	Leu Val Thr Glu Leu			
	1250		1255		1260
Asp Pro Ala Asp Pro	Val Leu Ala Ala Pro	Pro Thr Pro Ala Ala			
	1265		1270		1275
Pro Phe Ser Arg Phe	Thr Val Ser Pro Thr	Pro Ala Ser Arg Phe			
	1280		1285		1290
Ser Ile Thr His Ile	Ser Asp Ser Asp Ala	Gln Ser Val Gly Gly			
	1295		1300		1305
Pro Ala Ala Gly Ala	Gly Gly Arg Tyr Thr	Glu Ala			
	1310		1315		

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